Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/689,343_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _✓_ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _4_____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _✓_ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

RAW SEQUENCE LISTING ERROR REPORT

File Copy

BIOTECHNOLOGY SYSTEMS BRANCH
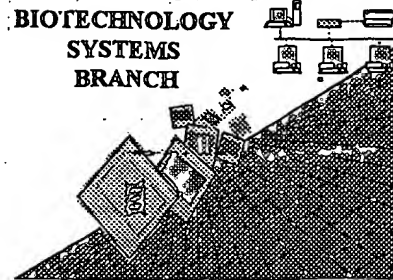
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/689,343*

Source: *OIPE*

Date Processed by STIC: *10/27/2000*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov **or phone 703-306-4119 (R. Wax)**
PATENTIN 3.0 e-mail help: patin30help@uspto.gov **or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING   DATE: 10/27/2000
PATENT APPLICATION: US/09/689,343   TIME: 08:36:04

Input Set : A:\Neb-181.app
Output Set: N:\CRF3\10272000\I689343.raw

Does Not Comply
Corrected Diskette Needed

```
 3 <110> APPLICANT: VAISVILA, ROMUALDAS
 4        MORGAN, RICHARD D.
 5        KUCERA, REBECCA B.
 6        CLAUS, TOBY E.
 7        RALEIGH, ELISABETH A.
 9 <120> TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE MseI RESTRICTION
10        ENDONUCLEASE
12 <130> FILE REFERENCE: NEB-181
14 <140> CURRENT APPLICATION NUMBER: US/09/689,343
15 <141> CURRENT FILING DATE: 2000-10-12
17 <160> NUMBER OF SEQ ID NOS: 9
19 <170> SOFTWARE: PatentIn Ver. 2.0
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22 <211> LENGTH: 903
23 <212> TYPE: DNA
24 <213> ORGANISM: Micrococcus sp.
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27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(900)
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37                 20                  25                  30
39 cga atg atc tac atc gat ccg ccg ttc aac aca ggg cga acg cag cgg   144
40 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
41             35                  40                  45
43 ctt cag tcg ctc aag acg acc cgc tcg gtc aca ggg tcg cga gtc ggc   192
44 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
45         50                  55                  60
47 ttc aaa ggc cag acg tac gac acg gtc aag agc act ctg cac tcg tat   240
48 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
49 65                  70                  75                  80
51 gac gac gct ttc acc gac tat tgg tcg ttc ctc gaa ccg cgt ctc ctg   288
52 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
53                 85                  90                  95
55 gag gct tgg cgg ttg ctc acc cct gac ggc gcg ctc tat ctt cat ctg   336
56 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
57             100                 105                 110
59 gat tac cgc gag gtt cac tac gcc aag gtc gtc ctc gac gcg atg ttc   384
60 Asp Tyr Arg Glu Val His Tyr Ala Lys Val Val Leu Asp Ala Met Phe
61         115                 120                 125
63 gga cgc gaa agc ttc ctg aac gag ctg atc tgg gcg tac gac tac ggc   432
64 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
65         130                 135                 140
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RAW SEQUENCE LISTING   DATE: 10/27/2000
PATENT APPLICATION: US/09/689,343   TIME: 08:36:04

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69 145             150             155             160
71 tat gtg aag gac ccg aac aac tac gtc tgg aac ggt cag gat gta gat    528
72 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
73                 165             170             175
75 cgc gag ccc tac atg gcg ccc ggg ctc gtt aca ccc gag aag gta gcg    576
76 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
77             180             185             190
79 ctt ggc aag ctg ccc acc gac gtc tgg tgg cac aca atc gtt ccg cct    624
80 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
81         195         .       200             205
83 gcg agc aaa gag cgc acc ggg tac gcg aca cag aag ccg gtc ggc atc    672
84 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
85     210             215             220
87 atc cgt cgc atg att cag gcg agc agc aat gaa ggc gac tgg gtt ctg    720
88 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
89 225             230             235         .   240
91 gat ttc ttc gct ggt agt ggg acg acc ggc gcc gcg gcc cgc cag ctc    768
92 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
93                 245             250             255
95 gga cgc cgt ttt gtg ctc gta gac gtc aac cca gaa gca atc gcg gta    816
96 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
97             260             265             270
99 atg gca aaa cgg ttg gat gac ggg gca ttg gac acc agc gtg acg atc    864
100 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
101         275             280             285
103 gtg cag act ccc cag agt gac cca cga acc gac gga tga               903
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105     290             295             300
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109 <211> LENGTH: 300
110 <212> TYPE: PRT
111 <213> ORGANISM: Micrococcus sp.
113 <400> SEQUENCE: 2
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117 Glu Ala Asp Asn Leu Asp Phe Ile Gln Thr Leu Pro Asp Ala Ser Phe
118             20              25              30
120 Arg Met Ile Tyr Ile Asp Pro Pro Phe Asn Thr Gly Arg Thr Gln Arg
121         35              40              45
123 Leu Gln Ser Leu Lys Thr Thr Arg Ser Val Thr Gly Ser Arg Val Gly
124     50              55              60
126 Phe Lys Gly Gln Thr Tyr Asp Thr Val Lys Ser Thr Leu His Ser Tyr
127 65              70              75              80
129 Asp Asp Ala Phe Thr Asp Tyr Trp Ser Phe Leu Glu Pro Arg Leu Leu
130             85              90              95
132 Glu Ala Trp Arg Leu Leu Thr Pro Asp Gly Ala Leu Tyr Leu His Leu
133         100             105             110
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136         115                 120                 125
138 Gly Arg Glu Ser Phe Leu Asn Glu Leu Ile Trp Ala Tyr Asp Tyr Gly
139         130                 135                 140
141 Ala Arg Ser Lys Ser Lys Trp Pro Thr Lys His Asp Asn Ile Leu Val
142 145                 150                 155                 160
144 Tyr Val Lys Asp Pro Asn Asn Tyr Val Trp Asn Gly Gln Asp Val Asp
145                 165                 170                 175
147 Arg Glu Pro Tyr Met Ala Pro Gly Leu Val Thr Pro Glu Lys Val Ala
148         180                 185                 190
150 Leu Gly Lys Leu Pro Thr Asp Val Trp Trp His Thr Ile Val Pro Pro
151         195                 200                 205
153 Ala Ser Lys Glu Arg Thr Gly Tyr Ala Thr Gln Lys Pro Val Gly Ile
154         210                 215                 220
156 Ile Arg Arg Met Ile Gln Ala Ser Ser Asn Glu Gly Asp Trp Val Leu
157 225                 230                 235                 240
159 Asp Phe Phe Ala Gly Ser Gly Thr Thr Gly Ala Ala Ala Arg Gln Leu
160                 245                 250                 255
162 Gly Arg Arg Phe Val Leu Val Asp Val Asn Pro Glu Ala Ile Ala Val
163                 260                 265                 270
165 Met Ala Lys Arg Leu Asp Asp Gly Ala Leu Asp Thr Ser Val Thr Ile
166         275                 280                 285
168 Val Gln Thr Pro Gln Ser Asp Pro Arg Thr Asp Gly
169         290                 295                 300
172 <210> SEQ ID NO: 3
173 <211> LENGTH: 1236
174 <212> TYPE: DNA
175 <213> ORGANISM: Unknown
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Unknown Organism: ENVIRONMENTAL DNA
180 <220> FEATURE:
181 <221> NAME/KEY: CDS
182 <222> LOCATION: (1)..(1233)
184 <400> SEQUENCE: 3
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186 Met Pro Thr Leu Asp Trp Pro Gly Lys Gln Leu Ser Phe Pro Pro Ala
187  1               5                  10                  15
189 acc tcc ttg cat ctg gag agt gtg gtc act gag gga gcg gag tca ccg    96
190 Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
191             20                  25                  30
193 cct aat cgt ctg att tgg gcg gac aac ctg ccg cta atg gta gat ttg   144
194 Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
195         35                  40                  45
197 ttg gcc gaa tat gaa ggg aaa atc gat ctg atc tac gcc gat ccc cct   192
198 Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
199         50                  55                  60
201 ttt ttt acg gat cgt act tat gcg gcg cga att ggt cat ggg gag gat   240
202 Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
203 65                  70                  75                  80
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RAW SEQUENCE LISTING   DATE: 10/27/2000
PATENT APPLICATION: US/09/689,343   TIME: 08:36:04

Input Set : A:\Neb-181.app
Output Set: N:\CRF3\10272000\I689343.raw

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     206 Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
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     209 tgg aag gat tta gat gaa tac ctg gac ttc ctt tat cca cgc ctg gta    336
     210 Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
     211            100                 105                 110
     213 ctg atg tat cga ctg ctg gca cca cac gga acg ctc tac ttg cac ctg    384
     214 Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
     215            115                 120                 125
     217 gac tgg cac gcc aat gcc tac gta cgt gta ctg ctt gat gag atc ttc    432
     218 Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
     219        130                 135                 140
     221 ggg cga cag cgg ttt ctc aac gag atc gtc tgg atc tat cac ggc ccc    480
     222 Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
     223 145                 150                 155                 160
     225 tca gcc atc cga cgc gcc ttc aag cgc aaa cat gat acc atc ttg gtt    528
     226 Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
     227            165                 170                 175
     229 tat gtg aaa ggt gaa aac tat aca ttc aat gcg gat gcg gtt cgt caa    576
     230 Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
     231            180                 185                 190
W--> 233 cct tac cat ccg agc ac  cat aag acc ttc gct tcc tcc ccg aag gcc    624
W--> 234 Pro Tyr His Pro Ser Xa  His Lys Thr Phe Ala Ser Ser Pro Lys Ala
     235            195                 200                 205
     237 ggc ttt ggt aag gtg ccg gat ctg cag cgc ggc aaa gtg ccc gaa gac    672
     238 Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
     239        210                 215                 220
     241 tgg tgg tat ttt ccg gtc gtg gcc cgt cta cac cga gaa cgg agc ggc    720
     242 Trp Trp Tyr Phe Pro Val Val Ala Arg Leu His Arg Glu Arg Ser Gly
     243 225                 230                 235                 240
     245 tat ccg act caa aag cct caa gcc ttg ctg gag cgg atc ctg ctg gcc    768
     246 Tyr Pro Thr Gln Lys Pro Gln Ala Leu Leu Glu Arg Ile Leu Leu Ala
     247            245                 250                 255
     249 tcc tcg aac gca ggc gat ctg gtg gca gac ttc ttc tgc ggc tca ggg    816
     250 Ser Ser Asn Ala Gly Asp Leu Val Ala Asp Phe Phe Cys Gly Ser Gly
     251            260                 265                 270
     253 aca acc gct gtg gtg gca gcc cgt ctg gga cgg cgc ttc ctg gtc aac    864
     254 Thr Thr Ala Val Val Ala Ala Arg Leu Gly Arg Arg Phe Leu Val Asn
     255            275                 280                 285
     257 gat gca agc tgg cgc gcc gtt cat gtg aca cgc aca cgc ttg cta cgc    912
     258 Asp Ala Ser Trp Arg Ala Val His Val Thr Arg Thr Arg Leu Leu Arg
     259        290                 295                 300
     261 gag gga gta agt ttc act ttt gaa cgc cag gaa act ttt act cta cct    960
     262 Glu Gly Val Ser Phe Thr Phe Glu Arg Gln Glu Thr Phe Thr Leu Pro
     263 305                 310                 315                 320
     265 atc cag cca ctt cca cca gat tgg ttg atc atc gcc gag gag cag att   1008
     266 Ile Gln Pro Leu Pro Pro Asp Trp Leu Ile Ile Ala Glu Glu Gln Ile
     267            325                 330                 335
     269 cgc ctc caa gca ccc ttt ctc gta gat ttt tgg gaa gtg gac gat caa   1056
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(handwritten, right margin) → see item 10 on Err Summary Sheet

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            RAW SEQUENCE LISTING              DATE: 10/27/2000
            PATENT APPLICATION:  US/09/689,343    TIME: 08:36:04

            Input Set : A:\Neb-181.app
            Output Set: N:\CRF3\10272000\I689343.raw

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271          340              345              350
273  tgg gat ggc aaa atc ttc cgc agc cgt cat caa ggc tta cgc tcc cgc   1104
274  Trp Asp Gly Lys Ile Phe Arg Ser Arg His Gln Gly Leu Arg Ser Arg
275          355              360              365
277  ctt cag gag cag gcg ccg ctc tct cta cca ttg acc ggg aat gga ctg   1152
278  Leu Gln Glu Gln Ala Pro Leu Ser Leu Pro Leu Thr Gly Asn Gly Leu
279          370              375              380
281  ttg tgt gta cgg gta gtg agc cgt gaa ggg gaa tac tat gag ttc aca   1200
282  Leu Cys Val Arg Val Val Ser Arg Glu Gly Glu Tyr Tyr Glu Phe Thr
283  385              390              395              400
285  ggt cga gcc gat agc cct cac ccc gta tcg ttt tga                   1236
286  Gly Arg Ala Asp Ser Pro His Pro Val Ser Phe
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291  <211> LENGTH: 411
292  <212> TYPE: PRT
293  <213> ORGANISM: Unknown
295  <220> FEATURE:
295  <223> OTHER INFORMATION:
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297  1               5               10              15
299  Thr Ser Leu His Leu Glu Ser Val Val Thr Glu Gly Ala Glu Ser Pro
300              20              25              30
302  Pro Asn Arg Leu Ile Trp Ala Asp Asn Leu Pro Leu Met Val Asp Leu
303          35              40              45
305  Leu Ala Glu Tyr Glu Gly Lys Ile Asp Leu Ile Tyr Ala Asp Pro Pro
306      50              55              60
308  Phe Phe Thr Asp Arg Thr Tyr Ala Ala Arg Ile Gly His Gly Glu Asp
309  65              70              75              80
311  Ser Arg Arg Pro Gln Thr Trp Gln Leu Ala Glu Gly Tyr Thr Asp Glu
312              85              90              95
314  Trp Lys Asp Leu Asp Glu Tyr Leu Asp Phe Leu Tyr Pro Arg Leu Val
315          100             105             110
317  Leu Met Tyr Arg Leu Leu Ala Pro His Gly Thr Leu Tyr Leu His Leu
318          115             120             125
320  Asp Trp His Ala Asn Ala Tyr Val Arg Val Leu Leu Asp Glu Ile Phe
321      130             135             140
323  Gly Arg Gln Arg Phe Leu Asn Glu Ile Val Trp Ile Tyr His Gly Pro
324  145             150             155             160
326  Ser Ala Ile Arg Arg Ala Phe Lys Arg Lys His Asp Thr Ile Leu Val
327              165             170             175
329  Tyr Val Lys Gly Glu Asn Tyr Thr Phe Asn Ala Asp Ala Val Arg Gln
330              180             185             190
332  Pro Tyr His Pro Ser Xaa His Lys Thr Phe Ala Ser Ser Pro Lys Ala
333          195             200             205
335  Gly Phe Gly Lys Val Pro Asp Leu Gln Arg Gly Lys Val Pro Glu Asp
336      210             215             220
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W--> 295 <220> FEATURE:
W--> 295 <223> OTHER INFORMATION:

→ see item 7 on Evo Summary Sheet

W--> 332

→ see item 10 on Evo Summary Sheet

VERIFICATION SUMMARY　　　　　　　DATE: 10/27/2000
PATENT APPLICATION: US/09/689,343　　TIME: 08:36:05

Input Set : **A:\Neb-181.app**
Output Set: **N:\CRF3\10272000\I689343.raw**

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:234 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:295 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:295 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:332 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:332 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:332 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:474 M:258 W: Mandatory Feature missing, <220> FEATURE:
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